



REPLACEMENT SHEET
Application No. 10/506,406, filed 3/14/05
Inventors: Swiercz et al.

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1 GAATTCTGCAGCTCAGCAGCCGCCAGAGCAGGACGAACGCCAATCGCAAGGCACC
 1 CTTAAGGACGTCGAGTCGTCGGCGGGTCTCGTCCCTGCTGGCGGTTAGCGTTCCGTGG
 61 TCTGAGAACCTCAGGATGCAGATGTCTCCAGCCCTCACCTGCCTAGTCCTGGGCCTGGCC
 61 AGACTCTTGAAGTCCTACGTCTACAGAGGTGGAGTGGACGGATCAGGACCCGGACCGG
 aa M Q M S P A L T C L V L G L A -
 |Signal Peptide
 121 CTTGTCTTGGTGAAGGGTCTGCTGTGCACCATCCCCATCCTACGTGGCCCACCTGGCC
 aa GAACAGAAACCACTTCCCAGACGACACGTGGTAGGGGGTAGGATGCACCGGGTGGACCGG
 aa L V F G E G S A |V H H P P S Y V A H L A 12
 Start Mature Protein
 181 TCAGACTTCGGGGTGAGGGTGTTCAGCAGGTGGCGCAGGCCTCCAAGGACCGAACGTG
 181 AGTCTGAAGCCCCACTCCCACAAAGTCGTCCACCGCGTCCGGAGGTTCTGGCGTTGCAC
 aa S D F G V R V F Q Q V A Q A S K D R N V 32
 241 GTTTCTCACCTATGGGGTGGCCTCGGTGTTGGCCATGCTCCAGCTGACAACAGGAGGA
 aa CAAAAGAGTGGGATACCCCACCGGAGGCCAACCCGGTACGAGGTCGACTGTTGTCCTCCT
 aa V F S P Y G V A S V L A M L Q L T T G G 52
 301 GAAACCCAGCAGCAGATTCAAGCAGCTATGGGATTCAAGATTGATGACAAGGGCATGGCC
 301 CTTTGGGTGTCGTCTAAGTTCGTCAACCTAAGTTCTAACTACTGTTCCCGTACCGG
 aa E T Q Q Q I Q A A M G F K I D D K G M A 72
 361 CCCGCCCTCCGGCATCTGTACAAGGAGCTATGGGCCATGGAACAAGGATGAGATCAGC
 361 GGGCGGGAGGCCGTAGACATGTTCCCTCGAGTACCCCGGTACCTGTTCCCTACTCTAGTCG
 aa P A L R H L Y K E L M G P W N K D E I S 92
 421 ACCACAGACGCGATCTCGTCCAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCAAC
 421 TGGTGTCTGCGCTAGAAGCAGGTGCGCCCTAGACTTCGACCAAGGTCCCGAAGTACGGGGTG
 aa T T D A I F V Q R D L K L V Q G F M P H 112
 481 TTCTTCAGGCTGTTCCGGAGCACGGTCAAGCAAGTGGACTTTCAAGAGGTGGAGAGAGCC
 481 AAGAAGTCCGACAAGGCCCTCGTGCCAGTTGTTCACCTGAAAGTCTCCACCTCTCGG
 aa F F R L F R S T V K Q V D F S E V E R A 132

FIG. 1A

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AGATTCATCATCAATGACTGGGTGAAGACACACACAAAAGGTATGATCAGCAACTTGCTT
541+.....+.....+.....+.....+.....+.....+.....+ 600
TCTAAAGTAGTAGTTACTGACCCACTTCTGTGTGTTTCATACTAGTCGTTGAACGAA
aa R F I I N D W V K T H T K G M I S N L L 152

GGGAAAGGAGCCGTGGACCAGCTGACACGGCTGGTGTGGTGAATGCCCTACTTCAAC
601+.....+.....+.....+.....+.....+.....+.....+ 660
CCCTTCCTCGGCACCTGGTCACTGTGCGGACACGACCACTACGGGAGATGAAGTTG
aa G K G A V D Q L T R L V L V N A L Y F N 172

GGCCAGTGGAAAGACTCCCTCCCCGACTCCAGCACCCACCGCCGCCTTCCACAAATCA
661+.....+.....+.....+.....+.....+.....+.....+ 720
CCGGTCACCTCTGAGGGAAAGGGGCTGAGGTGCGTGGTGGCGGGAGAAGGTGTTAGT
aa G Q W K T P F P D S S T H R R L F H K S 192

GACGGCAGCACTGTCTGTGCCATGATGGCTCAGACCAACAAGTTCAACTATACTGAG
721+.....+.....+.....+.....+.....+.....+.....+ 780
CTGCCGTCGTGACAGAGACACGGGTACTACCGAGTCTGGTTGTTCAAGTTGATATGACTC
aa D G S T V S V P M M A Q T N K F N Y T E 212

TTCACCACGCCGATGCCATTACTACGACATCCTGGAACGCCCTACACGGGACACC
781+.....+.....+.....+.....+.....+.....+.....+ 840
AAAGTGGTGCAGGGCTACCGGTAAATGATGCTGAGGACCTTGACGGGATGGTGCCTGTGG
aa F T T P D G H Y Y D I L E L P Y H G D T 232

CTCAGCATGTTATTGCTGCCCTTATGAAAAAGAGGTGCCCTCTCTGCCCTACCAAC
841+.....+.....+.....+.....+.....+.....+.....+ 900
GAGTCGTACAAGTAACGACGGGAATACTTTCTCCACGGAGAGAGACGGGAGTGGTTG
aa L S M F I A A P Y E K E V P L S A L T N 252

ATTCTGAGTGCCAGCTCATGCCACTGGAAAGGAAACATGACAGGCTGCCCGCCTC
901+.....+.....+.....+.....+.....+.....+.....+ 960
TAAGACTCACGGGTCGAGTAGTCGGTACCTTCCGGTTACTGGTCCGACGGGGCGGAG
aa I L S A Q L I S H W K G N M T R L P R L 272

CTGGTTCTGCCCAAGTTCTCCCTGGAGACTGAAGTCGACCTCAGGAAGCCCTAGAGAAC
961+.....+.....+.....+.....+.....+.....+.....+ 1020
GACCAAGACGGGTTCAAGAGGGACCTCTGACTTCAGCTGGAGTCCTCGGGGATCTCTTG
aa L V L P K F S L E T E V D L R K P L E N 292

CTGGGAATGACCGACATGTTCAGACAGTTCAGGCTGACTTCAGGAGTCTTCAGACCAA
1021+.....+.....+.....+.....+.....+.....+.....+ 1080
GACCCCTTACTGGCTGTACAAGTCTGTCAGGACTGAAGTGCTCAGAAAGTCTGGTT
aa L G M T D M F R Q F Q A D F T S L S D Q 312

FIG. 1B

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GAGCCTCTCACGTCGCGAGCGCTGCAGAAAGTGAAGATCGAGGTGAACGAGAGTGGC
1081+.....+.....+.....+.....+.....+.....+.....+ 1140
CTCGGAGAGGTGCAGCGCGTCCCGCACGTCTTCACTTCTAGCTCCACTTGCTCTCACCG
aa E P L H V A Q A L Q K V K I E V N E S G 332

ACGGTGGCCTCCTCATCCACAGCTGTCAAGTCTCAGCCGCATGGCCCCGAGGAGATC
1141+.....+.....+.....+.....+.....+.....+.....+ 1200
TGCCACCGGAGGAGTAGGTGTCGACAGTATCAGAGTCGGCGTACCGGGGGCTCTCTAG
aa T V A S S S T A V I V S A R M A P E E I 352

ATCATGGACAGACCCCTCCTCTTGTGGTCCGGCACAAACCCACAGAACAGTCCTTTTC
1201+.....+.....+.....+.....+.....+.....+.....+ 1260
TAGTACCTGTCTGGGAAGGAGAACACCAGGCCGTGTTGGGTGTCCTGTCAAGGAAAAG
aa I M D R P F L F V V R H N P T G T V L F 352

ATGGGCCAAGTGAATGGAACCCCTGACCCCTGGGAAAGACGCCCTCATCTGGGACAAAATG
1261+.....+.....+.....+.....+.....+.....+.....+ 1320
TACCCGGTTCACTACCTTGGGACTGGGACCCCTTCTGCGGAAGTAGACCCCTGTTTGAC
aa M G Q V M E P * 379

GAGATGCATGGAAAGAAGAAACTCCGAAGAAAAGAATTAGTGTAAATGACTCTTC
1321+.....+.....+.....+.....+.....+.....+.....+ 1380
CTCTACGTAGCCCTTCTTCTTGTAGGGCTCTTCTTAAATCACAATTACTGAGAAAG

TGAAGGAAGAGAACATTGCCTTTGTTAAAAGATGGTAAACCAGATCTGTCTCCAAG
1381+.....+.....+.....+.....+.....+.....+.....+ 1440
ACTTCCTTCTCTGTAAACGGAAAACAATTCTACCATTTGGTCTAGACAGAGGTTCTG
1441+.....+.....+.....+.....+.....+.....+.....+ 1500
ACCTTGGCCTCCCTGGAGGACCTTAGGTCAAACCTCCAGTCTCCACCTGAGACCCCT
TGGAACCGGAGAGGAACCTCCTGGAAATCCAGTTGAGGGATCAGAGGTGGACTCTGGGA
1501+.....+.....+.....+.....+.....+.....+.....+ 1560
GGGAGAGAACGTTGAAGCACAACCTCCCTAACGGTCTCCAAACCAGACGGTGACGCCCTGCG
CCCTCTCTCAAACCTCGTGTGTTAGGGAAATCCAGAGGTTGGTCTGCCACTGCGGACGC
1561+.....+.....+.....+.....+.....+.....+.....+ 1620
GGACCATCTGGGGCACCTGCTTCCACCCGCTCTCTGCCACTCGGGCTGAGACCTGG
CCTGGTAGACCCCGTGGACGAAGGTGGCAGAGAGACGGGTGAGCCAGACGTCTGGACC
1621+.....+.....+.....+.....+.....+.....+.....+ 1680
TTCCCACTGAGGCCCTTGCAGGATGGAACATCGGGCTTACAGGAGCTTGTGTGCCT
AAGGGTGACTCCGGAAACGTCCACCTGATGCCCGAATGTCCCTGAAAACACACGGA

FIG. 1C

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FIG. 1D

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FIG. 1E

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MQMSPALTCLVLGLALVFGEGLA
Signal Peptide

VHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQLTTGGETQQQIQA
AMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPFFRLFRST
VKQVDFSEVERARFIINDWKTHKGMIQNLLGKAVDQLTRLVLVNALYFNGQWKTPFP
DSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAP
YEKEVPLSALTNIQLSHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMDTDMFR
QFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASSSTAVIVSARMAPEEIIMDRPFLF
VVRHNPTGTVLFMGQVMEP

FIG. 2A

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10 20 30 40 50 60
| | | | | |
VHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQLTTGGETQQQIQA

70 80 90 100 110 120
| | | | | |
AMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRST

130 140 150 160 170 180
| | | | | |
VKQVDFSEVERARFIINDWVKHTKGMSNLLKGAVDQLTRLVLVNALYFNGQWKTPFP

190 200 210 220 230 240
| | | | | |
DSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAP

250 260 270 280 290 300
| | | | | |
YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFR

310 320 330 340 350 360
| | | | | |
QFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASSSTAVIVSARMAPEEIIMDRPFLF

370
|
VVRHNPTGTVLFMGQVMEP

FIG.2B

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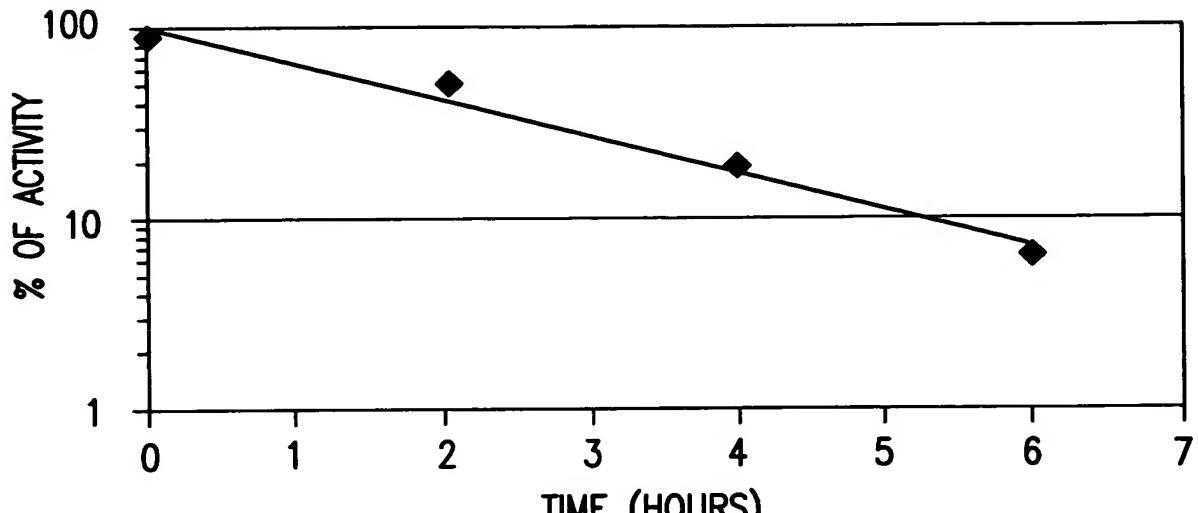


FIG.3

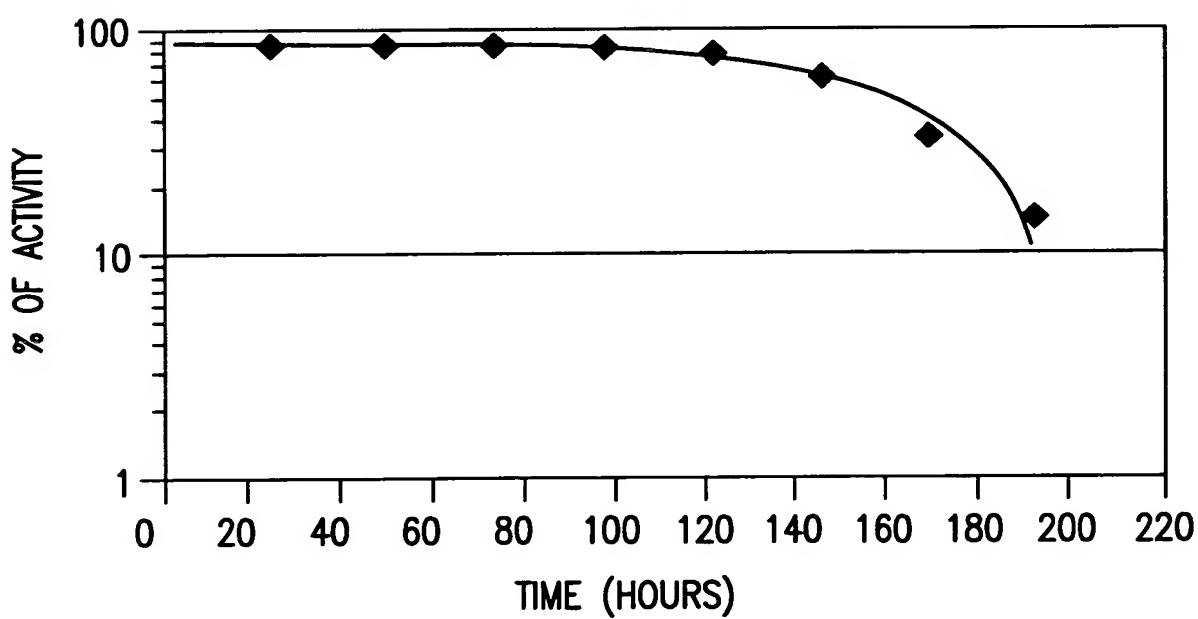


FIG.4

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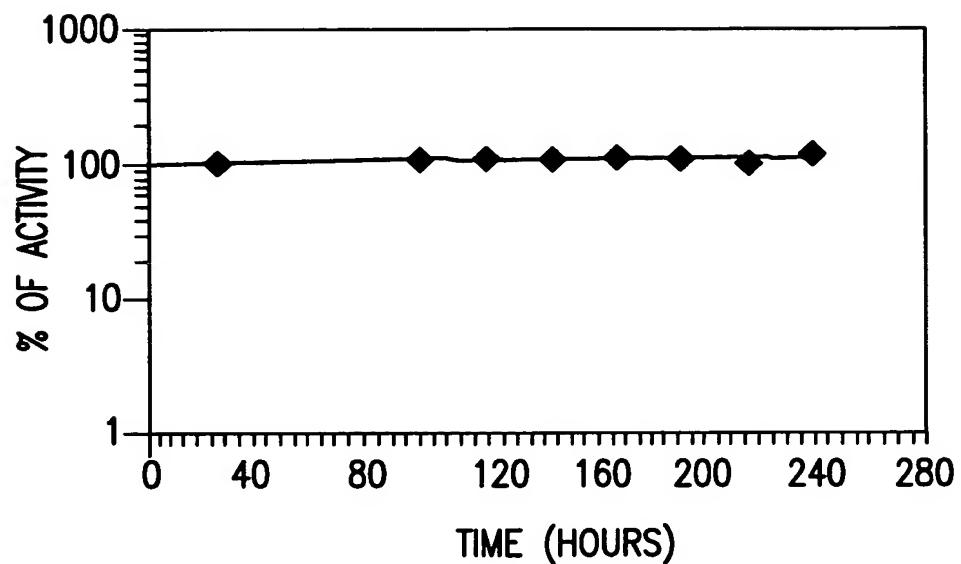


FIG.5

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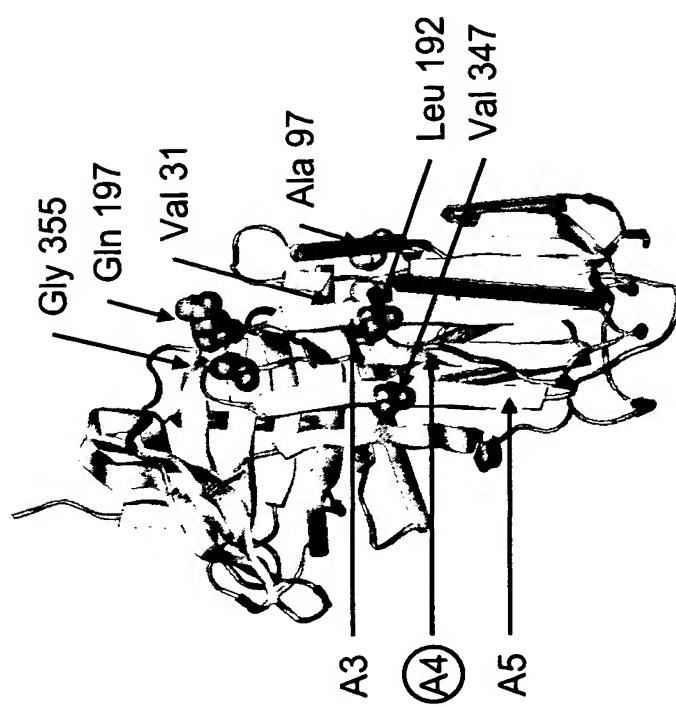
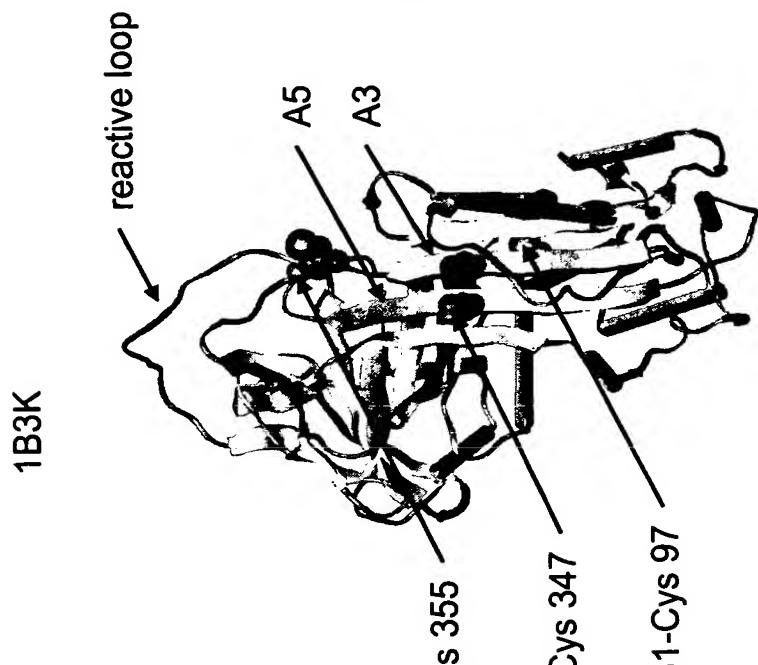


FIG. 6B

FIG. 6A

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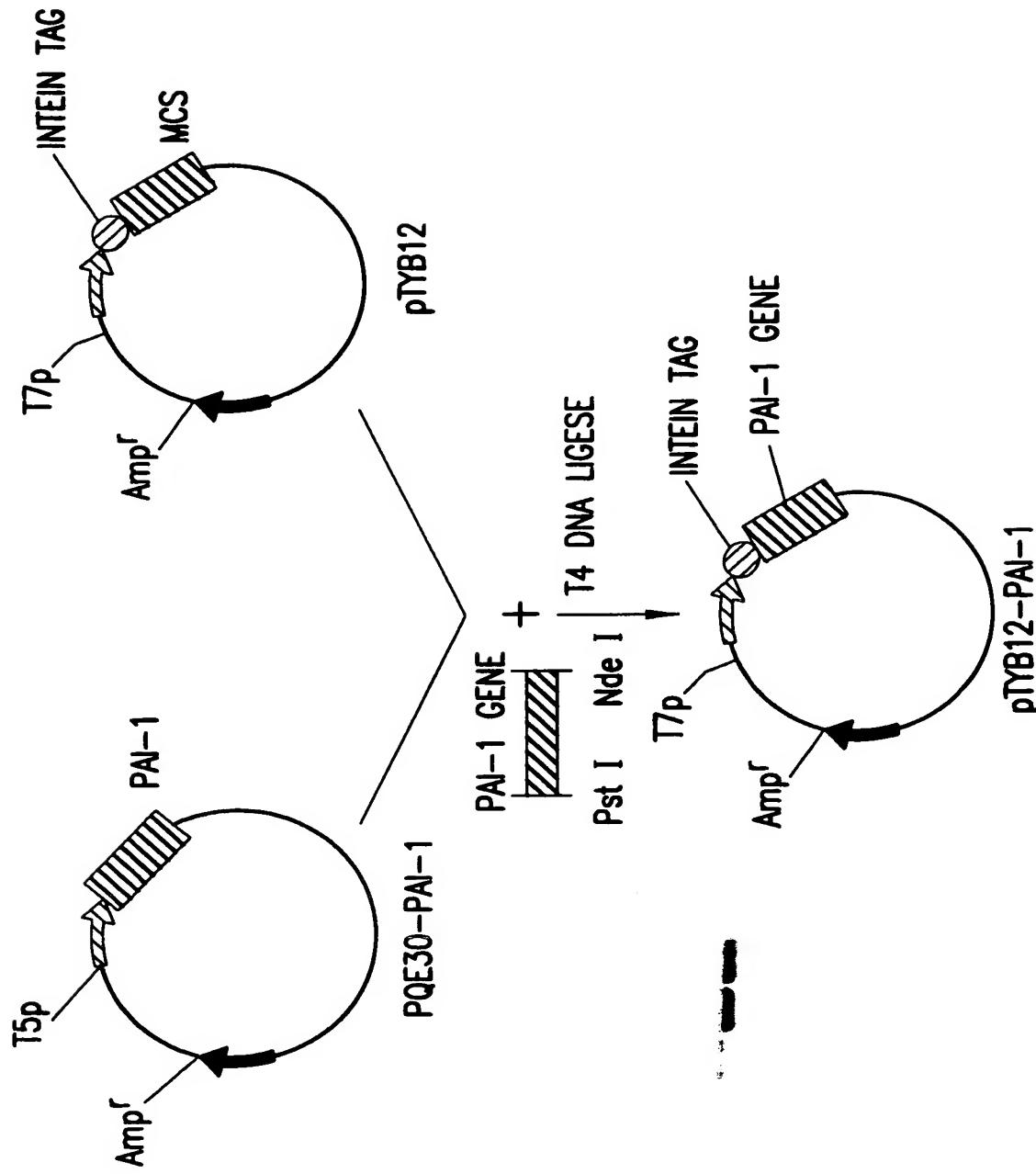


FIG. 7

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FIG.8A



FIG.8B

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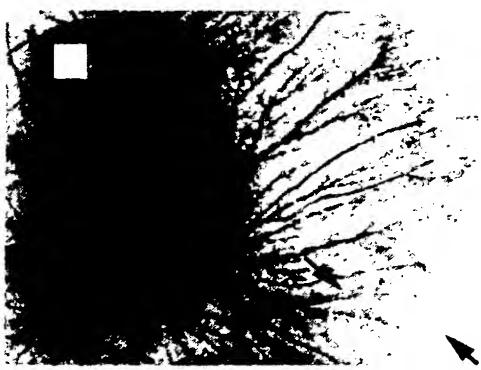


FIG.9A



FIG.9B

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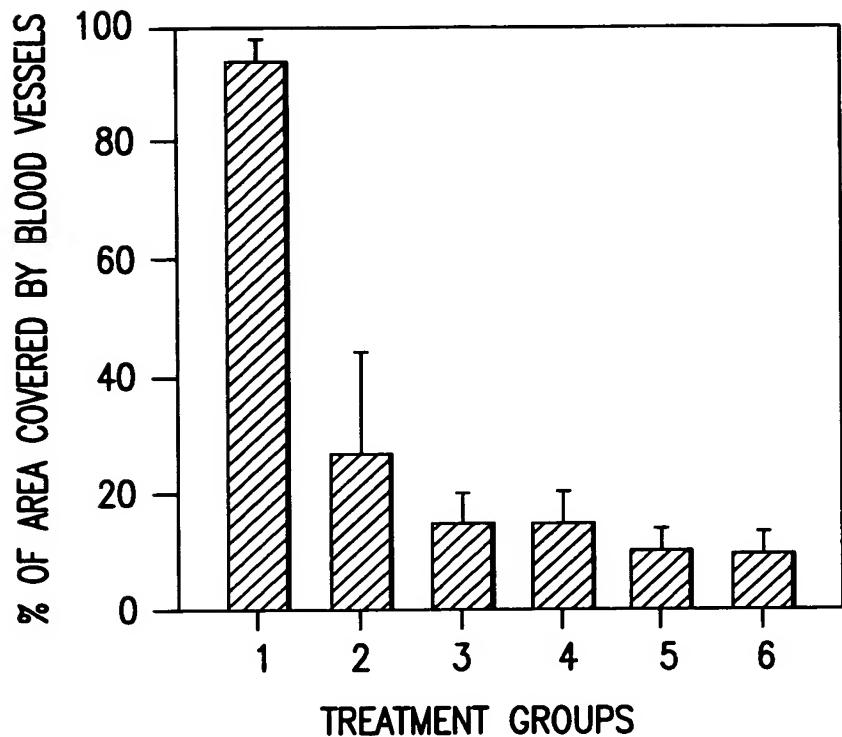


FIG. 10

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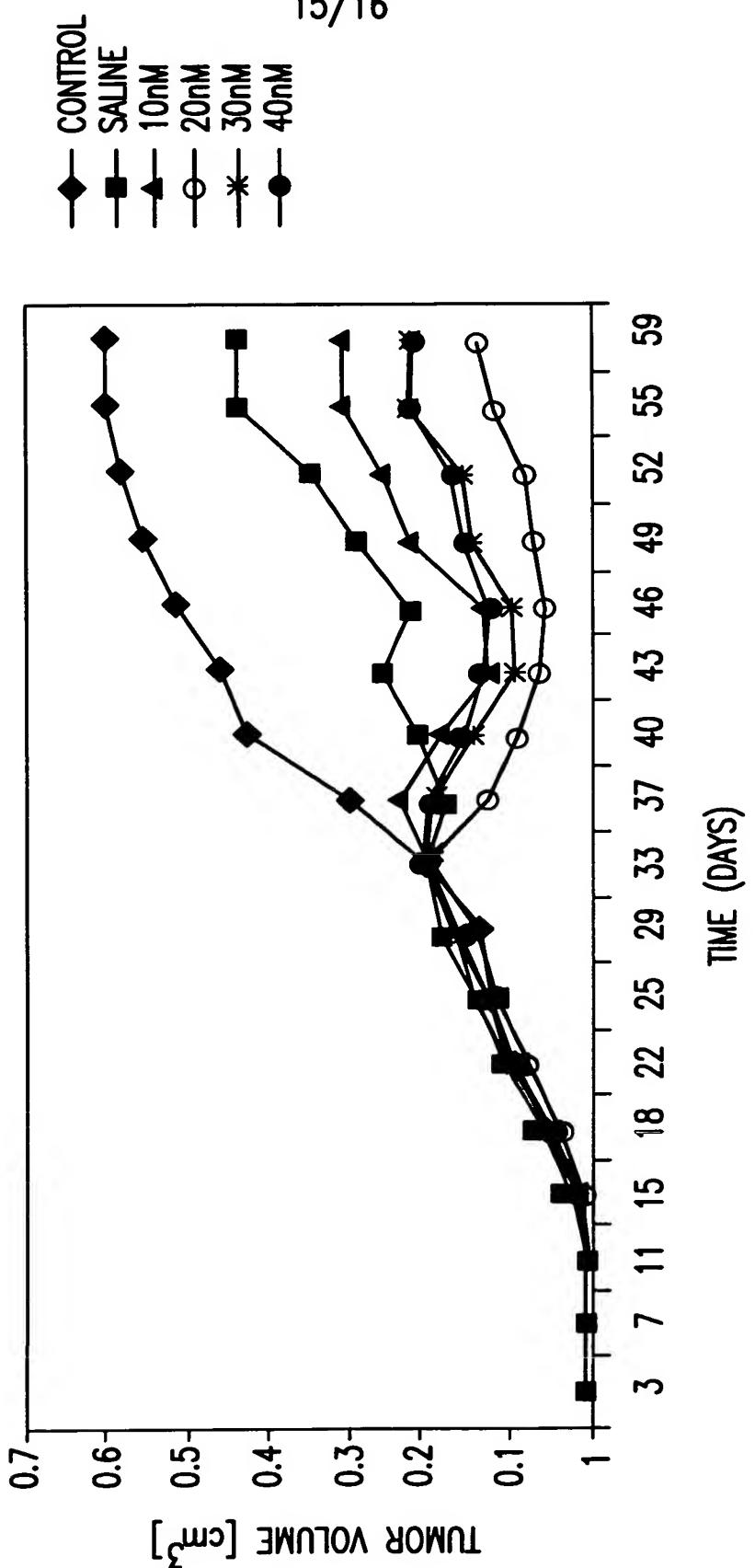


FIG. 11

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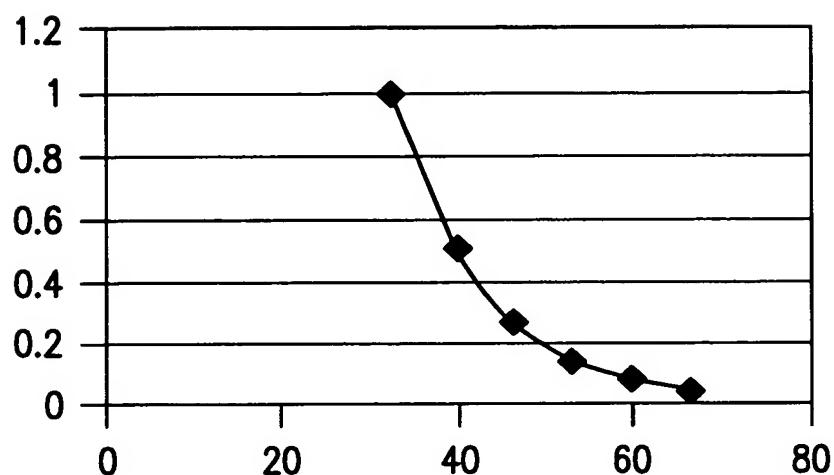


FIG. 12